STIC-Biotech/ChemLib

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Li, Bao-Qun

Sent:

Wednesday, April 28, 2004 7:54 AM STIC-Biotech/ChemLib

To:

Please do the sequence homology search for SEQ ID NO: 2 of application SN. 10,089,292. Thanks

Art unit 1648, REM, 3D24.

Tel. 20904

Searcher: Phone:_ Location: Date Picked Up: Date Completed: 4/29 Searcher Prep/Review:_ Clerical:_

Online time:_

THE OF SEARCH.
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

Other:_

ENDOR/COST (where applic.)
STN:	_
DIALOG:	
Questel/Orbit:	_
PRLink:	
Lexis/Nexis:	_
Sequence Sys.:	
WWW/Internet:	
Other (specify):	_

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5.1.6
Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

Run on:

April 28, 2004, 14:17:48 ; Search time 20 Seconds (without alignments) 1024.440 Million cell updates/sec

US-10-089-292A-2 1095

1 QLFYSRPVVSANGEPTVKLY......SLGAGPVSISAVALAPPPR 213 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	a	Description
7	1076	98.3	099	-	VHWWH2	structural protein
7	1043	95.3	629	Ч	B44212	structural protein
٣	91.5	8.4	1305	~	AB0168	probable cell divi
4	91.5	8.4		~	AB0821	
ß	90.5	8.3	261	~	S76484	
9	90	8.2	1045	~	A39199	a)
7	88	8.1	291	7	AH3391	biphenyl-2,3-diol
80	89	8.1	477	~	C70143	pyruvate kinase (p
σ	89	8.1	1802	~	S69703	HKR1 protein precu
10	88.5	8.1	665	~1	F95053	cell wall surface
11	88	8.0	583	~	867571	hypothetical prote
12	87	7.9	329	~	F87318	ㅁ
13	85.5	7.8	817	7	T01866	hypothetical prote
14	85.5	7.8	899	~	T16204	
15	85	7.8	292	~	AI1937	hypothetical prote
16	84.5	7.7	3	-	AJECDS	•
17	84.5	7.7	432	~	A98273	adenylosuccinate s
18	84.5	7.7	432	~	A86114	adenylosuccinate s
19	84.5	7.7	432	7	AF1049	adenylosuccinate s
20	83.5	7.6	253	~	C75611	transcription regu
21	83	7.6	288	~	T21732	ш
22	83	7.6	436	~	T03702	
23	83	7.6	269	~	C91195	
24	83	7.6	269	7	D86042	hypothetical prote
25	83	7.6	617	~	A56051	myocyte nuclear fa
26	83	7.6	765.	7	C64981	beta-glucosidase (
27	83	7.6	765	7	C91006	beta-D-glucoside g
28	83	7.6	765	~	D85850	beta-D-glucoside g
53	83	7.6	2422	7	T12687	ALR protein homolo

capsid protein - r ethanolamine utili	ethanolamine utili ethanolamine utili	coat protein - car Ig gamma-2a chain	hypothetical prote	probable PPE prote	translation elonga	Cellulase (EC 3.2. ABC transporter, p	conserved hypothet	racGAP protein - 8	hypothetical prote	chitinase (EC 3.2.
S22134 G85887	E65020 D91043	S52718 G2MSAB	AE1449	A70504	S09153	C2CLBM D90441	E89897	T18289	AF1972	T30418
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234	278 278	386 335	1946	394	418	563 693	868	1335	470	558
7.5	7.5	7.5	7.5	7.4	4.1	4. 4.	7.4	7.4	7.4	7.4
	ri ri	82.5	82	81	81	81	81	81	80.5	30.5
82.5 82.5	8 8 8 8	80	a						_	~

ALIGNMENTS

-4	
RESULT	VHWWH2

protein 2 precursor - hepatitis B virus (strain Burma) hepatitis B virus

C; Species: hepatitis E virus
C; Species: Jo-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
C; Accession: C40724
R; Taff, A.W.; Smith, M.W.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.F. Virology 185, 120-131, 1991
Virology 185, 120-131, 1991
A; Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vir A;Reference number: A40778; MUID:92024067; PMID:1926770

Affected to the state of the st

Gaps ö Length 660; 0; Indels Query Match

98.3%; Score 1076; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.1e-85;
Matches 210; Conservative 0; Mismatches 0;

ö

1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT g ð

513 61 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120 ò 셤

121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180 ઠે

g

181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210 574 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 603 ò g

RESULT 2/ B44212

Structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Species: hepatitis E virus
C;Accession: B44312
R;Huang, C;C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.; Virology 191, \$50=558=1292
A;Fitle: Molecular-cloning and sequencing of the Mexico isolate of hepatitis E virus (HEN A;Reference number: A44212; MUID:93079857; PMID:1448913

A; Accession: B44212

45;

Indels

Length 2130;

2;

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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 484-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Recessions. AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <-Par.
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA18613.1; PID:d1019346 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Genetics: A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Synechocysts sp.
A;Variety: PCC 6803
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: 876484
B;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, N.; Ass. 3; 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1291 PQPLAGR-----ITLISTLATDSDIQAVKAKN----SDSIPL--VITTTDAAGNP 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 EQDRPTPSPAPSRPFSVLRANDVLWLSL---TAAEYDQS-TYGSSTGPVYVSDSVTLVNV 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LFYSRPVVSANGE----PTVKLYTSVENAQODKGIAIPHDIDLG---ESRVVIQDYDNQH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 LIVSLPAIANNGSKQALPELQIHP------LPPELVDLGISLENRSLLGD-DGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSPAPSRPPSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYN-----TTASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VVSANGEPTVKLYTSVENAQODKGIAIPHD---IDLGES--RVV--IQDYDNQHEQDRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.3%; Score 90.5; DB 2; Length 261;
Best Local Similarity 23.6%; Pred. No. 2.2;
Matches 54; Conservative 32; Mismatches 74; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S76484
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-261 < KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GTAVLTLTQAAGPGVKNVITAALTDTP 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 OLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPP
                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.4%; Score 91.5; D
Best Local Similarity 24.4%; Pred. No. 28;
Matches 53; Conservative 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AB0168
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Jil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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A;Residues: 1-1305 <KUR>
A;Crosetics: GB:AL590842; PIDN:CAC90205.1; PID:g15979425; GSPDB:GN00175
C;Genetics:
A;Gene: ftsK
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                                                                                                                                                                                                                                                                                                                                                                               452
                                                                                                                                                                                                                                                                                                                                                                                                                                PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable cell division protein ftsk [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                             1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                                                                                                                                                                                                                              Gaps
                          A,Molecule type: genomic RNA
A,Residues: 1-659 «HUA»
A,Fresidues: 1-659 «HUA»
A,Cross-references: GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C,Superfamily: hepatitis E virus structural protein 2
C,Superfamily: hepatitis E virus structural protein 2
F;1-22/Domain: signal sequence #status predicted «SIG»
F;23-659/Product: structural protein 2 #status predicted «SP2»
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                                                                                                                                                                                                                          Query Match 95.3%; Score 1043; DB 1; Length 659; Best Local Similarity 94.3%; Pred. No. 3.6e-82; Matches 198; Conservative 9; Mismatches 3; Indels
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Best Local Similarity 27.9%;
Matches 38; Conservative
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Cypate kinase (pyk) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Reb-1998 #sequence_revision 13-Reb-1998 #text_change 18-Jun-1999
C;Accession: C70143
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Aitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Recession: C70143
A;Reternson C70143
A;Reternson crounder: A70100; MUID:98065943; PMID:9403685
A;Accession: C70143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001141; GB:AE000783; NID:g2688250; PIDN:AAC66733.1; PID:g2688256
A;Experimental source: strain B31
C;Superfamily: pyruvate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gubmitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 941(
A;Reference number: 869555
A;Accession: S69703
                                                                                                                           57 DRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVA-TGAQ 115
                                                                                                                                                                                                                                                   --KTFFVLPLRGKLSFWEAGTTKA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 ILTASGNPDVKIISKIENQEGIDNIEEIAKASYGIMVARGDMGVEIPAEDVPIAQLKITQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 TCIKYGIPVITATQMLHTMIENPRPTRAEVSDIANAILNGTDAIMLS-----GETAYGK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YPIEAVKM--MTSIAKKVEKHRKMTLYKDELFYDKSITRNYIIKCAIDATKLMDI 366
                                                                                                                                                                  ------ AQQDKGIAIP-HDIDLGESRV-- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 -----VIQDYDNQH----EQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $69703
HRKI protein precursor - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein YDR4.0w
C;Species: Saccharomyces cerevisiae
C;Dates: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001
C;Accession: S69703; A53382
                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 ----KAIIVDSLKGKTARIMA-TYRASVPL-FITTNSERLARELALSYGV 410
                                                                    42;
8.1%; Score 89; DB 2; Length 291;
26.5%; Pred. No. 3.5;
ive 15; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                      163 GYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Score 89; DB 2;
22.2%; Pred. No. 6.6;
tive 35; Mismatches 7
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                                                                                                                                                                                                                                                      116 AVARSLDWTKVTLDGRPLSTIQQYS
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Matches 51; Conservative
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1802 <DIE>
                                Local Similarity
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Query Match
Best Local S:
Matches 43
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biphenyl-2,3-diol 1,2-dioxygenase (EC 1.13.11.39) [imported] - Brucella melitensis (stra
C,Species: Brucella melitensis
C,Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                     Rimeinke, A.; Braun, C.; Gilkes, N.R.; Kilburn, D.G.; Miller Jr., R.C.; Warren, R.A.J. Bacteriol. 173, 308-314, 1991
A.Fitle: Unusual sequence organization in CenB, an inverting endoglucanase from Cellulom A;Reference number: A39199; MUID:91100298; PMID:1987122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1045 <MEI>
A;Cross-references: GB:M6464; NID:g144415; PIDN:AAA23086.1; PID:g144416
C;Superfamily: fibronectin type III repeat homology; bacterial cellulose-binding domain
C;Keywords: glycosidase; hydrolase
F;945-1045/Domain: bacterial cellulose-binding domain homology <BCB>
F;946-1044/Disulfide bonds: #status predicted
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A;Cross-references: GB:AE008917; PIDN:AAL52299.1; PID:g17983090; GSPDB:GN00190
A;Experimental source: strain 16M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APSRPFSVLRANDVLWLSLTAAE-----YDQSTYGSSTGPVYVSDSVTL----VN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 AGWNP----ANDPSYTGLTQTALAKASAITLYDGSTLVWGKEPTGTTDTTPPTTPGTP 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 YILRDLTPGTAYSYVVKAKDVAGNVSAASAAVTFTTDTTGETEPPTTPGTPVASAVTSTG 764
                                                                                                                                                                                                                                                endoglucanase B (EC 3.2.1.-) - Cellulomonas fimi
C;5pecies: Cellulomonas fimi
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 22-Oct-1999
C;Accession: A39199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDY----DNQHEQD---RPTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 VATGAQAVARSLDWTKVT----LDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2%; Score 90; DB 2; Length 1045; ilarity 26.3%; Pred. No. 15; Conservative 18; Mismatches 100; Indels 64; Gaps
                                                                    GTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVA
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;Keywords: oxidoreductase
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Best Local Similarity
Matches 65; Conserv
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A; Gene: CC0560
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Best Local S:
Matches 54
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A,Cross-references: EMBL:U33007; NID:g927685; PIDN:AAB64857.1; PID:g927691; MIPS:YDR420w, R;Kasahara, S.; Yamada, H.; Mio, T.; Shiratori, Y.; Miyamoto, C.; Yabe, T.; Nakajima, T. J. Bacteriol. 176, 1488-1499, 1994
A;Itle: Cloning of the Saccharomyces cerevisiae gene whose overexpression overcomes the A;Reference number: A53382; MUID:94156857; PMID:8113191
A;Reference number: A53382
A;Residues: 1-581, A, 583-593, A, 595-1802 < KAS>
A;Residues: 1-581, A, 583-593, A, 595-1802 < KAS>
A;Residues: 1-581, A, 583-593, A, 595-1802 < KAS>
A;Cross-references: EMBL:S69101; NID:g545659; PIDN:AAB30051.1; PID:g545660
A;Experimental source: YNN395
A;Gonetics: Sequence extracted from NCBI backbone (NCBIN:144410, NCBIP:144411)
C;Genetics: A;Genetics: A;Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVAR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUTSSE---LDNSIGE---LSTFILSYRSGSSTTTLSPKSISSLSW 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Conserveferences: SGD:S0002828; MIPS:YDR420w
A) Map position: 4R
C;Keywords: calcium binding; glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-2-1802/Product: HKR1 protein #status predicted <MAT>F;1483-1508/Domain: transmembrane #status predicted <TMM>F;1483-1508/Domain: calcium binding #status predicted <TMM>F;1645-1656/Domain: calcium binding #status predicted <CAl>Filess-1656/Domain: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1250 PINHTLITIGETAALNYVFLVQNPLSSAQ----IFNFLPLVLK----
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8.1%; Score 89; DB 2; Length 1802;
Best Local Similarity 26.3%; Pred. No. 38;
Matches 44; Conservative 24; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VTLDGRPLST-----IQQYSKTFFVLPLRGKLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
8.1%; Score 88.5; DB
Best Local Similarity 26.9%; Pred. No. 11;
Matches 42; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
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Cispecies: Caulobacter crescentus
Cispecies: Capr-2001 #sequence_revision 20-Apr-2001 #text_change 28-Jul-2003
Cispecession: R8718
E. Heidelberg, J. Heidelberg, J. Heidelberg, J. Heinerman, W. C.; Feldhlyum, T. V.; Paulsen, T. T.; Dodson, R. J.; Durkin, A. S.; Gwinn, M. L.; Haft, D. H.; Kolons
n, J.; Ermolaeva, M.; White, O.; Salzberg, S. L.; Shapiro, L.; Venter, J. C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S. A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Fraser, C. M. A. S. A. S. MUID: 21173698; PMID: 11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-583 <PAU>
A;Cross-references: EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023; GSPDB:GN00004;
A;Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 SLTDMVSSTGSADLSVSSIQRSQVDPSTFAVSNSPVXPTASTG--STSTGIPIASBSLSL 433
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                                                                                                                                                                                                                                                                                                                                                 C.Species: Saccharomyces cerevisiae)
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C.Accession: 867571
R.Paulin, L., Saren, A.M.; Laamanen, P.
Submitted to the Protein Sequence Database, July 1996
A.Reference number: 867560
A.Accession: 867571
A.Molecule V.Ppe: DNA
A.Reference T. A.Reference Database, July 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 583
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DB 2;
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A;Gene: MIPS:YDL038c
A;Cones: MIPS:YDL038c
A;Crosoltences: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin
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hes 54; Conservative
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hypothetical protein alr1052 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: Al1937
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Feference number: Ab1807; MUID:21595285; PMID:11759840
                  A; Residues: 1-899 <PAU>
A; Residues: 1-899 <PAU>
A; Cross-references: EMBL:U00045; NID:g470353; PID:g470357; PIDN:AAA50684.1; CESP:F28F5.3
A; Experimental source: strain Bristol N2
C; Genetics: CESP:F28F5.3
A; Gene: CESP:F28F5.3
A; Introns: 22/3; 41/3; 54/3; 72/2; 129/3; 182/3; 307/3; 365/1; 444/3; 525/3; 632/3; 674/3
C; Superfamily: Caenorhabditis elegans hypothetical protein F28F5.3
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                  457 PVMSARVEATFKOPPPREGVKPFVSRAAQD----ITHN----GESKVENIDLTIELNREQK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 ATVTATKYPRTDFIMEDY---HRPQTQILAPAPKKPNSTTRIYHAVDIPFDESPASYYPK 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 TYGSSTGPVYVSDSVTLVNVATGAQAVARSLD----WTKVTLDGRPLSTIQQYSKTFFV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KTEFV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                          46 -----VIQDYDNQHEQDRPTPSPAPSRPFSVLR---ANDVLWLSLTAAEYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 RVVIQDYDNQHEQDRPTPSPA-------PSRPFSVLRANDVLWLSLTAAEYDQS
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                                                                                                                                                                                                                            Query Match 7.8%; Score 85.5; DB 2; Length 899; Best Local Similarity 24.4%; Pred. No. 30; Matches 41; Conservative 20; Mismatches 54; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.8%; Score 85; DB 2; Length 292; 25.5%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 ---STTTP----SATLGNENNANSÄVÄVTLELQGNSWLQVTADG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LPL-RGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAIS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GELTKGDRRTW------TAKKQLTVRSGNAGAVLVS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                    7 PVVSANGEPTVK-----LYTSVENAQODKGIAIPHDIDLGESRV
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Best Local Similarity 25.5%; Pred. No. 7.7;
Matches 42; Conservative 18; Mismatches
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A.Molecule type: DNA
A.Residues: 1-292 <KUR>
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A;Introns: 117/3; 188/2; 269/3; 307/3; 357/3; 395/3; 422/3; 447/1; 486/3; 513/3; 541/3;
A;Note: T24M8.3
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                                                                                                                                                                                                                                                                                       101 VSDSVTLVNVATGAQAVARSLDWTK-----VTLDGRPLSTIQQYSKTFFVLP----L 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EAGTTK----AGYPYNYNTTASDQLLVENAAGH----RVAISTYTTSLGAG----PVSI 202
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                                                   71 VLRANDVLWLSLTAAEYDQSTYGSS-----------TGPVYVSDSV 105
AQGGWMVRAVTSFRISRPERPRIAPSDLAAASSLV----ESWAAEEAGRVTPVAQRPDS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F28F5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C;Accession: T16204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ypothetical protein T24M8.3 - Arabidopsis thaliana
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LFYSRPVVSANGEPTVKLYTSVENAQ-----QDKGIAIPHDIDLG--ESRVVIQDYDNQ
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Best Local Similarity 22.7%; Pred. No. 27;
Matches 44; Conservative 36; Mismatches 71; Indels 43; Gaps
                                                                                                                                                106 TLVNVATGA--QAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFW-----
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A;Cross-references: EMBL:AF077409; NID:g3319365; PID:g3319369
A;Experimental source: cultivar Columbia
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submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid F28F5.
A;Reference number: Z18477
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Libmitted to the EMBL Data Library, August 1998
Pescription: The sequence of A. thaliana T24M8, Reference number: Z14449
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STRAIN-2B Abbottabad;
STRAIN-2B Abbottabad;
Wan Cuyck-Gandre H., Clements N.J., Zhang H.Y., Caudill J.C.,
Cohen S.G., Coursaget P., Buisson Y., Warren R.L., Longer C.F.;
"Partial Sequence of HEV Isolates from North Africa and Pakistan:
Comparison with Known HEV Sequences.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40044; AADD9445.1;
GO; GO:0005198; F:structural molecule activity; IEA.
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NON TER 1
SEQÜENCE 344 AA; 37146 MW; D7F3D2D9BB44098B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; seRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=12461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA.
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Q8JJM8
Q91114
Q8V729
Q80IR7
Q81861
Q8JW3
Q8JJM2
Q8JJN2
Q8JJN2
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Q81860
Q9YPB0
Q9W9E8
  Query Match
Best Local Similarity 100.0
Matches 210; Conservative
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                                                                                      April 28, 2004, 14:17:13; Search time 45 Seconds (without alignments) 1493.453 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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               van Cuyck-Gandre H., Zhang H.Y., Tearev S.A., Warren R.L.,
Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
"Phylogenetically distinct hepatitis E viruses in Pakistan.";
Am. J. Trop. Med. Hyg. 62:187-189 (2000).
EMBL; AF18582; AAG16766.1; -
GO; GO:0005198; E:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; I.
SEQUENCE 660 AA; 70903 MW; IF506BE3CFB3BACE CRC64;
                                                                                                                                                                                                                                98.3%; Score 1076; DB 12; Length 660; 100.0%; Pred. No. 2.7e-89; ive 0; Mismatches 0; Indels 0
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
structural protein 2 (Structural viral protein).
Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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 MEDLINE=20271579; PubMed=10813471;
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Matches 210; Conservative
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C STRAIN-BON;

X MEDLINE-99013657; PubMed-9797311;

RD Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;

RT "Characterization of a strain of infectious hepatitis E virus isolated
RT from sewage in an area where hepatitis E is not endemic.";

RL Appl. Environ. Microbiol. 64:4485-4488(1998).

DR EMBL; APC08684; AAC77808.1; -.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR004261; SP2.

DR InterPro; IPR008975; Viral_cap_coat.

DR Pfam; PF03014; SP2.

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                     198 LDWTKVTLDGRPLSTIQQYSKIFFVLPLRGKLSFWEAGTTKAGYPYNYNTASDQLLVEN 257
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98.3%; Score 1076; DB 12; Length 605;
Best Local Similarity 100.0%; Pred. No. 2.4e-89;
Matches 210; Conservative 0; Mismatches 0; Indels 0
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein (Fragment).
Hepatitis E virus.
Viruses, seRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TAXID=12461;
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                           181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                                 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 287
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Hepatitis E virus.
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SEQUENCE FROM N.A.
STRAIN=Abb-2B;
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Q9E8G5;
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Q9E8G5
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ö of Gaps M Chen G., Meng J.;
"Identification of the 5' Capped and 3' Complete Terminal Sequence the Hapaticis E virus Isolated From Morocco.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065061; AAD10627.1; -.
EMBL; AX230202; AAO72992.1; -.
GO; GO:0005198; F:structural molecule activity; IEA. "Primary structure of open reading frame 2 and 3 of the hepatitis virus isolated from Morocco."; J. Med. Virol. 57:126-133(1999). ö STRAIN=HEV-Morocco; MEDLINE=99107414; PubMed=9892396; Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A., Khudyakov Y.E.; Length 660; Indels InterPro; IPR004261; SP2. InterPro; IPR008975; Viral_cap_coat. Pfam; PF03014; SP2; 1. SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;

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61 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
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MEDLINE=95176571; PubMed=7871758;
Yin S., Purcell R.H., Emerson S.U.;
"A new Chinnese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
Virus Genes 9:23-32(1994).
                                                                                                                                                        Donati M.C., Fagan B.A., Harrison T.J.;
"Sequence analysis of full length HEV clones derived directly from "Sequence analysis of full length HEV clones derived directly from Muman liver in fulminant hepatitis B.";
(In) Rizzetto M., Purcel R.H., Gerin J.L., Verme G (eds.);
VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316,
Edizioni Minerva Medica, Torino (1997).
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                                                                                                                                                                                                                                                                                                       Harrison T.J.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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the EMBL/GenBank/DDBJ databases.
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
                                                              Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=12461;
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 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Structural protein.
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Matches 208; Conservative
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Yin S.R., Purcell R.H.,
Submitted (MAR-1996) to
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QLFYSRPVVSANGEPTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                  394 QLFYSRPVVSANGEPTVKLYTSVENAQOKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
"Reevaluation of a North India isolate of hepatitis E virus based o
the full-length genomic sequence obtained following long RT-PCR.";
Virus Res. 86:33-58(2002).
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SEQUENCE FROM N.A.
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, F4FS9438; AAM66330.1;
GO; GO:0005199; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
NCBI_TaxID=12461;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; 125547; AAA91080.1; -.
EMBL; L25595; AAA65490.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004975; P.P.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PP03014; SP2; 1.
SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA stage;
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Last annotation update)
                                                                                                                                                                                                                                                                                                      97.9%; Score 1072; DB 12;
99.5%; Pred. No. 6.38-89;
ive 0; Mismatches 1;
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99.5%; Pred. No. 6.3e-89;
iive 0; Mismatches 1
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Hepatitis E-like viruses.
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InterPro; IPR008975; Viral_cap_coat.
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
ORF-2.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.5'
Matches 209; Conservative
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Matches 209; Conserv
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61 PSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
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MEDLINE=991-EGYPt;
MEDLINE=99106430;
MEDLINE=99106430;
MEDLINE=99106430;
Van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
"Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
"Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
J. Med. Virol. 57:68-74(1999).
EMBL; ARO51351; AAC35761.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR0048261. SP2.
InterPro; IPR0048975; Viral_cap_coat.
Efam; PF03014; SP2; 1.
SEQUENCE 660 AA; 71040 MW; 044FF5EA7C492791 CRC64;
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MEDLINE=99105430;
PubMed=9890424;
Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis B virus isolates from Egypt.";
J. Med. Virol. 57:68-74(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=12461;
                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-2998 (TrEMBLrel. 08,
01-OCT-2003 (TrEMBLrel. 25,
Structural protein.
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Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno K., Win K.M.;
"Hepatitis E virus: cDNA cloning and expression.";
Microbiol. Immunol. 36:67-79(1992).
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TBarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
Malik I.A., Iqbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
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Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T., Zhuang H.,
Win K.M.;
                                                                                        97.8%; Score 1071; DB 12; Length 99.0%; Pred. No. 7.7e-89; Artive 1; Mismatches 1; Indels
EMBL; AF051352; AAC35764.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
SEQUENCE 660 AA; 71026 MW; 16C560FA16941F2A CRC64;
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Hepatitis E-like viruses.
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MEDLINE=92024067; PubMed=1926770;
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MEDLINE=92271462; PubMed=1589964;
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Virology 185:120-131(1991).
                                                                                        Query Match
Best Local Similarity 99.03
Matches 208; Conservative
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Pry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M., Platak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A., Bradley D.W., Reyes G.R., "Hepatitis B virus (HEV): Strain variation in the nonstructural gene region encoding consensus motifs for an RNA-dependent RNA polymerase virus Genes 6:173-185(1992).
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Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 660 AA; 70979 MW; B58F23955FDD6614 CRC64;
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SEQUENCE 660 AA; 70937 MW; 5412313F1A2EF4A9 CRC64;
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Hepatitis E virus.
Viruses; septitive-strand viruses, no DNA stage;
NCBI_TaxIb=12461;
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GO; GO:0005198; F:structural molecule activity; IEA
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Hepatitis E virus.
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                                                                                                             PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF051830; ASC97188.1; ...
GO, GO:00005199; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfan; PPG3014; SP2; Viral_cap_coat.
SEQUENCE 660 AA; 70798 MW; A04C0185ACC085DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; serNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
NCBL TaxID=12461;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Capsid protein.
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STRAIN=TK15/92;
MEDLINE=99049628; PubMed=9833882;
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Van Chyck-Gandre H., Caudill J., Clements N., Zhang H., Buisson Y.,

Van Chyck-Gandre R., Longer C.;

Cohen S., Warren R., Longer C.;

Estination of HV isolate from Chad outbreak 1983.";

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, U62121, AABG1825.1;

ENBL, GO. 0005198; R:structural molecule activity; IEA.

InterPro; IPR004261; SP2.

InterPro; IPR008975; Viral_cap_coat.
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llarity 99.0%; Pred. No. 2.2e-88;
Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 1067; DB 12; Length 525; 98.6%; Pred. No. 1.3e-88; tive 1; Mismatches 2; Indels 0
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X99441; CAA67804.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      525 AA; 56594 MW; 9AFEF48C206351C8 CRC64;
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                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NOV-1996 (TYEMBLYEL: 01, C3
01-NOV-1996 (TYEMBLYEL: 01, L6
01-OCT-2003 (TYEMBLYEL: 25, L6
ORF1, ORF2 & ORF3.
Hepatitis E virus.
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Best Local Similarity 98.6°
Matches 207; Conservative
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SEQUENCE 660 AA; 709
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Best Local Similarity
Matches 208; Conserv
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181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
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US-08-240-049B-13
Sequence 13, Application US/08240049B
Patent No. 5686239
GENERAL INFORMATION:
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US-09-172-699-18
US-09-172-699-18
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-840-316-2
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US-08-477-292-15
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, David A.
APPLICANT: Anderson, David A.
APPLICANT: Accarnini, Stephen A.
APPLICANT: Coresi, Joseph
APPLICANT: Hui, Zhuang
APPLICANT: Hui, Zhuang
TITLE OF INVENTION: IMMUNOREACTIVE ANTIGENS OF HEPATITIS E VIRUS
FILE REFERENCE: Davies COl. Cave
CURRENT APPLICATION NUMBER: US/09/172,699A
CURRENT FILING DATE: 1998-10-14
EARLIER FILING DATE: 1996-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                       Sequence
                       Sequence
Sequence
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98.3%; Score 1076; DB 4; Length 2
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 210; Conservative 0; Mismatches 0; Indels
US-08-478-507-8

US-08-842-634-13

US-08-142-634-13

US-09-128-275-8

US-08-471-971-2

US-08-477-292-13

US-09-462-606-12

US-09-462-606-12

US-09-462-606-12

US-09-462-606-12

US-09-172-699-2

PCT-US93-08849A-2

PCT-US93-08849A-2

PCT-US95-13703-13

US-09-462-606-53

US-09-462-606-53
                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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; Patent No. 6514690 ,
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PSPAPSRPFSVLRANDVLMLSLTAABYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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                APPLICANT: Tam, Albert W.
APPLICANT: Yarbough, Patrice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
NUMBER OF SEQUENCES. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis E Virus (Burma strain) SG3
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-MAY-1994
CLASSIFICATION: 435
TURNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REGISTRATION INFORMATION:
TELECOWGUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
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                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
Yarbough, Patrice D.
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-259-148A-15; Sequence 15, Application US/08259148A; Patent No. 5741490...); GENERAL INFORMATION: APPLICANT: Bradley, Daniel W.
                                                                                                                                       STREET: 505 Penobscot Drive CITY: Redwood City
Reyes, Gregory R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 327 amino acids
amino acid
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Best Local Similarity 100.
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-240-049B-13
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usa
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
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IITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.3%; Score 1076; DB 1; Length 3 100.0%; Pred. No. 4.4e-104; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
RICHA APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRICK APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
US-08-259-148A-15
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                     NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMUNICATION INPORMATION:
TELEPANE: (415) 324-0860
INFORMATION FOR SEC ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-OCT-1989
FILING DATE: 13-OCT-1989
PAPPLICATION DATA:
APPLICATION NUMBER: US 367-48F
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 420,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 327 amino acids
amino acid
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                                                                                                                Palo Alto
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                                                                                                                                                           COUNTRY:
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61 QLFYSRPUVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT 120
                                                                                                                                 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
                                                                                                                                                                                             121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Mitchell, Garl
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
TITLE OF INVENTION: Antibodies
NUMBER OP SEQUENCES: 76
CORRESPONDENCE ASSOCIATES
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          241 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 270
                                                                                                                                                                                                                                                                                           181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
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CUKRENT APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 17-JAN 1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 13-OCTOBER-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION DATE: 16-JUNE-1989
PRIOR APPLICATION DATE: 18-JUNE-1989
PRIOR APPLICATION DATE: 18-JUNE-1989
PRIOR APPLICATION DATE: 1909
PRIOR APPLICATION DATE: 1909
PRIOR APPLICATION DATE: 1909
PRIOR APPLICATION DATE: 11-APRIL-1989
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FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 38,615
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEO ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RY: USA
94306
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                                                                                                                                      APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.-Shin
APPLICANT: Twu, Jr.-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: / 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNFOR: US/08/484,054
FILING DATE: 07-UUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
CRIGINAL SOURCE:
INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
US-08-484-054-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR AFFILIATION NUMBER: US 822,335
PRIOR APPLICATION NUMBER: US 822,335
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 4600-0093.38
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
                                                                    pplication US/08484054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING CVCMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 amino acids
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Best Local Similarity 100.
Matches 210; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: //
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; INDIVIDUAL ISOLATE: region US-08-542-634-17
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APPLICANT: Yacbough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                       ö
                                                                                                                                                                              Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
                                                                                                                                                                                                                     Indels
                                                                                                                                                                              98.3%; Score 1076; DB 2; L 100.0%; Pred. No. 4.4e-104; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG3, BURMA, FIGURE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATONEY AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET.NUMBER: 4600-0293.30
TELECHOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Ave., Suite 250 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-542-694-17, Application US/08542634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fuerst, Thomas R.
                                                                                                                                                                                                                       Conservative
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                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                        ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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Best Local Similarity
Matches 210; Conserva
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                                                                                                                                       US-07-876-941A-15
                                       TOPOLOGY:
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61 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
                                                                                                                                                                                                      121 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 180
                                                                                                                61 QLFYSRPVVSANGEPTVXLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                              1 OLFYSRPVVSANGEPTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                          Gaps
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Length 327;
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Query Match 98.3%; Score 1076; DB 3; L
Best Local Similarity 100.0%; Pred. No. 4.4e-104;
Matches 210; Conservative 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
                                                                                                                                                                                                                                                                                                                                 181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                                                                                                                                                                                                                                                                                                       241 AAGHRVAISTYTTSLGAGÞVSISAVAVLAP 270
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,952
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION VINGHER: 36,373
REFERENCE, DOCKET NUMBER: 632P5
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                 121 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 180
                                                                                                                                                                                                                                                                              LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                        61 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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       DB 3; Length 327; 4.4e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                     181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                                                                                                                                                                                                                                                                                                                               AAGHRVAISTYTTSLGAGPVSISAVAVLAP 270
    98.3%; Score 1076; Dilarity 100.0%; Pred. No. 4.4 Conservative 0; Mismatches
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STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R. REGISTRATION VMBER: 33,875
REGISTRERNCE/DOCKET NUMBER: 4600-0093.30
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APPLIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Application US/07870985A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 345592
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Pwu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
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ATTORNEY/AGENT INFORMATION:
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Query Match
Best Local Similarity
Matches 210; Conserv
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61 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIFHDIDLGESRVVIQDYDNQHEQDRPT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 240
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                                                                                                                                                                                                                                                                                         Length 327;
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                                                                                                                                                                                                                                                                                           98.3%; Score 1076; DB 4; I
100.0%; Pred. No. 4.4e-104;
ive 0; Mismatches 0;
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MEDIUM TYPE: R.Loppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
FILING DATE:
                                                                                                                                                                                                                         SG3, BURMA, FIGURE 9
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NAME: Fabian, Gary R.
REGISTRAINON WOMBER: 34875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEFAK: (415) 324-0860
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: USBS THEREFOR
NUMBER OF SECURNICES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: Deblinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application PC/TUS9513703 GENERAL-INFORMATION:
APPLICANT:
(415) 324-0880
              TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                       : 327 amino acids
amino acid
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TYPE: amino acid
                                                                                                                                                                                                                                                                                       Query Match 98.34
Best Local Similarity 100.0
Matches 210; Conservative
                                                                                                                                                  MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INIVIDIAL ISOLATE: S
US-07-870-985A-15
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
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; Sequence 17,
; Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                  121 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LDWIKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTIKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                     1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                                                                                                                                               Gaps
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APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                      98.3%; Score 1076; DB 5; Length 327; 100.0%; Pred. No. 4.4e-104; tive 0; Mismatches 0; Indels
Hepatitis E Virus (Burma strain) SG3
region
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COMPUTER: IBM PC compatible
ODERATING SYSTEM:
COMPUTER: IBM PC compatible
ODERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Rolease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
PRIOR APPLICATION NUMBER: US 208,997
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                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 210; Conservative
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                         ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
PCT-US95-13703-17
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170 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 PSPAPSRPFSVLRANDVLMLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 IDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTASDQLLVEN 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bradley, Deniel W.
APPLICANT: Bradley, Deniel W.
APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Twn, Albert W.
APPLICANT: Trawczynski, Krzysztof Z.
APPLICANT: Trawczynski, Krzysztof Z.
CORRESPONDENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.3%; Score 1076; DB 1; Length 4: Best Local Similarity 100.0%; Pred. No. 6.7e-104; Matches 210; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPY disk
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
PRICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRICATION NUMBER: US 870,335
PRICATION NUMBER: US 822,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
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                                                                                                                                                                                                                                                                                                                                                                                C2, BURMA, FIGURE
                REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELERAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08484054
$770689
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Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
Charles K
                                                                                                                                                                                                                  LENGTH: 436 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-259-148A-17
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APPLICANT: Reyes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTASDQLLVEN 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLFYSRPVVSANGEPTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Mitchell, Carl
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
98.3%; Score 1076; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.7e-104;
Matches 210; Conservative 0; Mismatches 0; Indels
                                     APPLICATION NUMBER: US 420,921
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 336,672
PRIOR APPLICATION NUMBER: US 208,997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFRAM: (415) 324-0960
INFORMATION POR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TENATTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 379
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-484-054-17
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170 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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98.3%; Score 1076; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.7e-104;
Matches 210; Conservative 0; Mismatches 0; Indels (
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PELICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 367,786
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
RICH APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
RICH APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-870-985A-17
; Sequence-17, Application US/07870985A
; Patent No. 6455492
; GREERAL-LUFORMA-TON:
APPLICANT: Reyes, Gregory R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein uvportHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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290 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 349
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                                                                                                                                                                           US-08-542-634-27
; Sequence 27, Application US/08542634
; Patent No. 6214970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FABLIAN, GALY R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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                                       APPLICANT: Twu, Jr-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Twu, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Krawczynski, Krzysztof Z.
CORRESPONDENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                     OPERATION SYSTEM: PC-DOS/MS-DOS OFFRANTUS SYSTEM: PC-DOS/MS-DOS OFFTANTOS SYSTEM: PC-DOS/MS-DOS OFFTANTOS DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/870,985A FILING DATE: 20-APRIL-1992 CLASSIFICATION NUMBER: US 822,335 FILING DATE: 17-JAN-1992 PRIOR APPLICATION NUMBER: US 505,888 FILING DATE: 17-JAN-1992 PRIOR APPLICATION NUMBER: US 505,888 FILING DATE: 05-APRIL-1990 PRIOR APPLICATION NUMBER: US 367,486 FILING DATE: 13-OCTOBER-1989 PRIOR APPLICATION NUMBER: US 367,486 FILING DATE: 16-UNNE-1989 PRIOR APPLICATION NUMBER: US 367,486 FILING DATE: 11-APRIL-1989 PRIOR APPLICATION NUMBER: US 367,786 FILING DATE: 11-APRIL-1989 PRIOR APPLICATION NUMBER: US 36,672 FILING DATE: 11-APRIL-1989 PRIOR APPLICATION NUMBER: US 208,997 FILING DATE: 17-UNNE-1988 ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33.875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 17:
                     Daniel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 210; Conservative
                     Bradley, Dan:
Twu, Jr-Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                         USA
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121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
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                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: MARCHE, C. Patrick
APPLICANT: Yarbough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 525;
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98.3%; Score 1076; DB 3; Length 5
Best Local Similarity 100.0%; Pred. No. 8.8e-104;
Matches 210; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis E virus (Burma strain)
r62kDa, 56.5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/542,634 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                         350 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 379
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
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STRANDEDNESS: single | TOPOLOGY: linear | TOPOLOGY: linear | TOPOLOGY: linear | TOPOLOGY: protein | HYPOTHETICAL: NO | ORIGINAL SOURCE: | INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain) | INDIVIDUAL ISOLATE: r62kDa, 56.5 kDa | PCT-US95-13703-27
                           Sequence 27, Application PC/TUS9513703
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCES:
ADDRESSE: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0840
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
RESULT 15
PCT-US95-13703-27
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0; Gaps Query Match
98.3%; Score 1076; DB 5; Length 525;
Best Local Similarity 100.0%; Pred. No. 8.8e-104;
Matches 210; Conservative 0; Mismatches 0; Indels

121 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180 403 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 462 ò 원

Search completed: April 28, 2004, 14:22:28 Job time : 23 secs

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LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWBAGTTKAGYPYNYNTTASDQLLVEN 180
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                                                                                                         April 28, 2004, 14:16:38 ; Search time 18 Seconds (without alignments) 616.164 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                141681 seqs, 52070155 residues
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HRR1_YEAST
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92561377; PubMed=1584074;
MCDLida T., Suzuki K., Hayaahi N., Iida F., Hara T., Oo S.S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1060; DB 1; Length 4
Pred. No. 1e-84;
1; Mismatches 2; Indels
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                                                      Structural protein 2 (Fragment).
Hepatitis B virus (isolate Rhesus) (HEV).
Viruses; SENRA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                "Hepatitis E virus: cDNA cloning and expression."; Microbiol. Immunol. 36:67-79(1992).
01-0CT-1993 (Rel. 27, Last sequence update) 01-0CT-1993 (Rel. 27, Last annotation update)
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last sequence update)
Structural protein 2 precursor (ORF2)...
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InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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Best Local Similarity 98.6%;
Matches 207; Conservative
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514 LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 573
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TRACTOR S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J., Malik I.A., Igbal M., Purcell R.H.; Enarcy S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J., Malik I.A., Igbal M., Purcell R.H.; Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).

-I- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 660;
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660 AA; 70980 MW; 8085BC53CF846FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus (strain Pakistan) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.3%; Score 1076; DB 1;
Best Local Similarity 100.0%; Pred. No. 6.2e-86;
Matches 210; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                   660 AA.
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                                                               181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                             574 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 603
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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ID VST2_HEVRH STANDARD;

AC Q00270;

DT 01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                      STANDARD;
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660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                          RESULT 2

NETT HEVPA

10 -VST2 HEVPA

AC P33426;
DT 01-FEB-1994
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Gaps

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Length 485;

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381
                                                                  LDWTKVTLDGRPLSTIOOYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                   PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS
                                 322 PSPAPSRPFSVIRANDVLWLSLTAAEYDQSTYGSSTAPVYVSDSVTLVNVATGAQAVARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93227573; Pubwed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
"Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                            orinculai procein & precursor (ukr.).
Hepatitis B virus (strain Myanmar) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
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Virus Genes 7:95-109(1993)
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RESULT 3

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23 6
659 AA;
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Q8ZGC7;
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                                                                                                                        SEQUENCE
                                                                                                                                                    Query Match
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLPYSRPVVSANGEPTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,
Bradley D.W., Tam A.W., Reyes G.R.,
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 191:550-558(1992).
-!- FUNCTION: CONTENIS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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                                                                                                                                                                                                                                                                                  / Match 96.8%; Score 1060; DB 1; Length 660; Local Similarity 98.6%; Pred. No. 1.5e-84; hes 207; Conservative 1; Mismatches 2; Indels (
                                                                                                                                                                                                                              1 22 BY SIMILARITY.
23 660 STRUCTURAL PROTEIN 2.
660 AA; 70998 MW; 3A82A4EA255C6253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus (strain Mexico) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 AA.
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                                                                                                                                                                          InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93079857; Pubmed=1448913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor.
                                                                                                                                                              EMBL; D10330; BAA01174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31768;
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                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                  Signal.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 PSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARS 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVEN 180
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MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomeon N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Hollroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPT
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J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: DNA motor protein, which is both required to move lout of the region of the septum during cell division and for septum formation. Tracks DNA in an ATP-dependent manner by generating positive supercoils in front of it and negative
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                      95.3%; Score 1043; DB 1; Length 659; 94.3%; Pred. No. 4.6e-83; ive 9; Mismatches 3; Indels (
                                                                                                                                                                                                                                                  STRUCTURAL PROTEIN 2. CF75E75EFD8FBE2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 AAGHRVAISTYTTRLGAGPVAISAAAVLAP 602
                                                                                                                                                                                                                  BY SIMILARITY
EMBL; M74506; AAA45732.1; -.
PIR; B44212; B44212.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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STRAIN=KIMS / Biovar Mediaevalis;
                                                                                                                                                                                                              22 BY
659 ST
70640 MW;
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FTSK OR YPO1376 OR Y2800.
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.3
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                           Pfam; PF03014; SP2; 1.
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Braun C., Gilkes N.R., Kilburn D.G., Miller R.C. Jr.,
      Meinke A., Bran
Warren R.A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P26221;
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                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715 APTQP-----VVTSASAIST 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
         supercoils behind it. Also plays a role in resolution of dimer chromosomes by regulating the xerC and xerD recombination complex, possibly by switching the catalytic state of the two recombinases. Required for the targeting of ftsD, ftsL and ftsI to the septum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 EPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSP-----
                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Located at the
septum. The large C-terminal part of the protein is cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase B)
                                                                                                                                   (By similarity). SUBUNIT: Homohexamer. This suggests the formation of a ring between the two cells at the septum that surrounds DNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ414148; CAC90205.1; -.
EMBL; AE013883; AAM86350.1; -.
PIR, AB0168; AB0168.
HAMAP; MF 01809; -; 1.
InterPro; IPR002543; FreK SpoiliE.
Pfam; PF01580; FreK SpoiliE; 1.
PROSITE; PS50901; FTEK; 1.
Chromosome partition; Cell division; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
Local Similarity 27.9%; Pred. No. 6.6;
Les 38; Conservative 17; Mismatches 40; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 966 973 ATP (POTENTIAL).
1305 AA; 140681 MW; DD25C959541F1839 CRC64;
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                                                                                                                                                                                                                                                                                                                   (Potential).
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SVTPTSIASLNTAPVS 773
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P26225;
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NP BIND
SEQUENCE
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GUNB_CEL
ID GUNB CF
AC P2625,
DT 01-MAY.
DT 01-MAY.
DT 01-MAY.
DT 28-FEB.
DE Endolib
E Cellul,
CO CELLUL
CO MICTOCC
OC MICT
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococcineae, Cellulomonadaceae, Cellulomonas.

Cellulomonas fimi

NCBI_TaxID=1708;

[1] SEQUENCE FROM N.A. MEDLINE=91100298; PubMed=1987122;

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                                                                                                                                                                                                                                                                                                                   Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
Meinke A., Gilkes N.R., Kilburn D.G., Miller B.C. Jr., Warren R.A.J.;
Thurtiple domains in endoglucanase B (CenB) from Cellulomonas fimi:
Thurtions and relatedness to domains in other polypeptides.";
Thurtions and relatedness to domains in other polypeptides.";
T. J. Bacteriol. 173:7126-7135 (1991).

C. I. FUNCTION: The biological conversion of cellulose to glucose
C. Generally requires three types of hydrolytic enzymes. (1)
Exocellobiohydrolases that cut the dissaccharide cellobiose
C. Endoglucanases which cut internal beta-1,4-glucosidic bonds;
C. Endoglucanases which hydrolyze the cellulose polymer chain; (3)
Exocellobiohydrolases which hydrolyze the cellobiose and other
short callo-Oligosaccharides to glucose.
C. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucans.
C. Inkages in cellulose, lichenin and cereal beta-D-glucans.
C. Inkages in cellulose, lichenin and cereal beta-D-glucans.
C. Inkages in cellulose, lichenin and cereal beta-C-glucans.
C. INSCELLANBOUS: The linker region (also termed "hinge") may be a potential site for proteolysis.
C. I. MISCELLANBOUS: MAX CONTAIN A SECOND CBD IN THE CATALYTIC DOMAIN.
C. I. SIMILANITY: Contains 3 fibronectin type III domains.
C. I. SIMILANITY: Belongs to cellulase family E (family 9 of glycosyl
                                                           "Unusual sequence organization in CenB, an inverting endoglucanase from Cellulomonas fimi.";
J. Bacteriol. 173:308-314(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKER ("HINGE") (PRO-THR BOX).
CELLULOSE-BINDING (BY SIMILARITY).
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BY SIMILARITY.
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W; ACZF7B84E4E3C4F0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKER ("HINGE")
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                                                                                                                                                                                                                                                                 DOMAINS.
MEDLINE=92041609; PubMed=1938913;
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SGD; S0002828; HKR1
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P41809;
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                                                                      APSRPFSVLRANDVLWLSLTAAE-----YDQSTYGSSTGPVYVSDSVTL----VN 109
                                                                                                                                   503 AGWNP-----ANDPSYTGLTQTALAKASAITLYDGSTLVWGKEPTGTTTDTTPPTTPGTP 657
                                                                                                                                                               110 VATGAQAVARSLDWTKVT----LDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKA-- 162
                                                                                                                                                                                          658 VATGVTTVGASLSWAASTDAGSGVAGYELYRVQGTTQTL-------VGTTTAAA 704
                                                                                                                                                                                                                   -----GYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVS----ISAV---- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIREATCS 35210 / B31;
STRAIREATCS 35210 / B31;
STRAIREATCS 35210 / B31;
Braser C.M., Casjens S., PubMed=9403685;
Fraser C.M., Casjens S., Hunng W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J. F., Rielschmann R.D., Richardson D., Peterson J., Kerlavage A.F., Quackenbush J., Salzberg S., Hanson M., van Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artlach P., Bowman C., Garland S., Fuji C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                       ANGEPTUKLYTSVENAQODKGIAIPHDIDLGESRVVIQDY----DNQHEQD---RPTPSP
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).

-!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
-!- COPACTOR: Requires magnesium and potassium.
-!- PATHWAY: Glycolysis; final step.
-!- PATHWAY: Glycolysis; final step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the pyruvate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                            64;
 DB 1; Length 1045;
8.2%; Score 90; DB 1; Length 104
26.3%; Pred. No. 6.7;
ative 18; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
18-EBB-2003 (Rel. 41, Last annotation update)
Pyruvate kinase (RC 2.7.1.40) (PK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001697; Pyruvate_kinase.
Pfam; PP00224; PK; 1.
Pfam; PF02887; PK_C; 1.
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                          Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                         206 AVLAPPP 212
                                                                                                                                                                                                                                                                                                   765 ATLAWAP 771
              Similarity
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 STGPVYVSDSVTLVNVATGAQAVARSLDWT-------KVTLDGRPLSTI 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VIQDYDNQH---EQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGS
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--- FUNCTION: Could regulate beta-glucan synthesis. Overexpression provides resistance to HW-1 killer toxin.
--- SUBCELGLAR LOCATION: Type I membrane protein (Probable).
--- FTM: Could be O-glycosylated in the serine/threonine-rich domain.
--- SIMILARITY: SOME, TO YEAST MSB2.
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MEDLINE=94156857; PubMed=8113191;
Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
Yabe T., Nakajima T., Ichishima E., Furuichi Y.;
"Cloning of the Saccharomyces cerevisiae gene whose overexpression overcomes the effects of HM-1 killer toxin, which inhibits
beta-glucan synthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 OQYSKTPFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hansenula MRAKII killer toxin-resistant protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.1%; Score 89; DB 1; Length 477; 22.2%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                     MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                            40D3CCAC9ACB7D98 CRC64;
Prodom; PO1009; PYRUVATENASE.
TIGREMA; TIGRO1064; PYRUVATE Kinase; 1.
PROSITE; PS00110; PYRUVATE KINASE; 1.
Pyruvate; Transferase; Kinase; Glycolysis; Magnesium; Complete proteome.
AT 214
METAL
214
214
316
216
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Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                         216 216 MAC
237 237 MAC
238 238 MAC
477 AA; 53032 MW; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1250 PINHTLITIGFTAALNYVFLVQNPLSSAQ----IFNFLPLVLK--------YPF 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SLDWTKVT------LDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
                                                                                                                                                                                                        12 X 28 AA TANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-À-P-A-A-I-S-S-T-
                                    POTENTIAL.
HANSENULA MRAKII KILLER TOXIN-RESISTANT
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Enterobacteriaceae; Escherichia.
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10-OCT-2003 (Rel. 42, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 89; DB 1; Length 1802;
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J. Biol. Chem. 263:19147-19153(1988).
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PURA OR ADEK OR B4177 OR C5261 OR Z5784 OR ECS5153
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STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
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Glycoprotein; Transmembrane;
SIGNAL 1 21
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Escherichia coli O6, and
Escherichia coli O157:H7.
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SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MARTIO R., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Iida T., Takami H., Honda T., Baharo I., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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"T. T. T. And qenomic Comparison with a laboratory strain K-12.";
                                                                                                                                                                 MEDLINE=22388234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 145-147, AND MUTAGENESIS OF ARG-147.
MEDLINE-91286237; PubMed=2061308;
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J. Biol. Chem. 266:12228-12233 (1991).
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Poste D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postei G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Melch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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sequence in Escherichia coli adenylosuccinate synthetase.";
J. Bioll. Chem. 257:2388-2392(1992).
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MEDLINE=96095802; PubMed=7490761;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                 STRAIN=06:H1 / CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                   of uropathogenic Escherichia coli.
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MEDLINE=97443975; Pubmed=9298646;
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PDB; 1QF5; 0
PDB; 1CG0; 1
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MUTAGEN
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Choe J.Y., Poland B.W., Fromm H.J., Honzatko R.B.;
"Mechanistic implications from crystalline complexes of wild-type and
mutant adenylosuccinate synthetases from Escherichia coli.";
Silva M.M., Poland B.W., Hoffman C.R., Fromm H.J., Honzatko R.B.; "Refined crystal structures of unligated adenylosuccinate synthetase from Escherichia coli.";
                                                                                                                     MEDIJNE=97153337; PubMed=9000627;
Poland B.W., Fromm H.J., Honzatko.R.B.;
"Crystal structures of adenylosuccinate synthetase from Escherichia coli complexed with GDP, IMP hadacidin, NO3-, and Mg2+.";
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                                                                                                                                                                                                                                                                                                              adenylosuccinate.
-!- COFACTOR: Binds 1 magnesium ion per subunit.
-!- PATHWAY: AMP biosynthesis; first committed step.
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                                         (2.6 ANGSTROMS).
                                                                                                                  K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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                         J. Mol. Biol. 254:431-446(1995).
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                                        X-RAY CRYSTALLOGRAPHY
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08-NOV-96.
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                                                                                                                                                         DR BCOGene; EG10790; purA.

DR HAMAP, MF 00011; -; 1.

DR HAMAP, MF 000114; Asucc synthtase.

DR ProDom; P0001189; Asucc synthtase.

DR ProDom; P0001089; Asucc synthtase; 1.

DR PTGRAMS; TIGR00184; purA; 1.

DR PROSITE; PS00513; ADENYLOSUCCIN SYN 2; 1.

DR PROSITE; PS00513; ADENYLOSUCCIN SYN 2; 1.

DR PROSITE; PS01266; ADENYLOSUCCIN SYN 2; 1.

DR PROSITE; PS01266; ADENYLOSUCCIN SYN 2; 1.

DR PROSITE; PS01266; ADENYLOSUCCIN SYN 2; 1.

TINT MET 0 0 GTP (POTENTIAL).

TACT SITE 140 140 PROBABLE.

TH ACT SITE 147 147 PROBABLE.

TH METAL 13 13 MAGNESIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGNESIUM.
MAGNESIUM (VIA CARBONYL OXYGEN).
G->V: SIGNIFICANT REDUCTION IN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenyloguccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 84.5; DB 1; Length 431; 24.3%; Pred. No. 6.5; ive 29; Mismatches 73; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 LLVENAAGHRVA-----ISTYTTSLGAGP 199
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Salmonella typhimurium, and
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
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                                              05-APR-00.
20-MAR-02.
20-MAR-02.
                                                                                                                                    20-MAR-02.
17-JUN-99
                     29-DEC-99
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BIFLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MBDLINE=22531367; PubMed=12644504; MBDLINE=22531367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R., "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2.
                                                                                                                                                                SPECIES-S. Urphi; STRAIN-CT18; MEDLINE-21534947; PubMed=11677608; MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Plays an important role in the de novo pathway of purine nucleotide biosynthesis.
-!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
                           'Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICRFAMS; TICRO0184; pura, 1. Proceeds to the process of the proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenylosuccinate.
-!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-!- PATHWAY: AMP biosynthesis; first committed step.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELDULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the adenylosuccinate synthetase family.
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GTP (POTENITAL).

BY SIMILARITY.

BY SIMILARITY.

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (VIA CARBONYL OXYGEN) (BY
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Pfam; PF00709; Adenylsucc_synt; 1.
ProDom; PD001188; Asucc_synthtase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE008905; AAL23186.1; -. EMBL; AL627283; CAD06843.1; -. EMBL; AE016849; AA071866.1; -.
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                                                                                   Nature 413:852-856(2001).
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HAMAP; MF (
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11;

73; Indels 57; Gaps

28 QDKGIAIPHDIDLGESRVVIQDY----DNQHEQDRPTPS-----PAPSRPFSV---L 72

24.3%; Pred. No. 6.5; ative 29; Mismatches

51; Conservative

Matches

Local Similarity

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RANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRP 132
                                                                                                                                                                                                                                     147 RVGDL------FDKETFAEKLKEVMEYHNFQLVNYYK----AEAVDYQKVLDDTMA 192
                                                                                                                                                                                                                                                                                                                                  133 LSTI------QQYSKTPFVL--PLRGKLSFWEAGTTKAGYPY--NYNTTASDQ 175
                                                                                                                                                                                                                                                                                                                                                                                             :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UD-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berg
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: Glycolysis.
-1- SUBUMIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Cytcoplesmic (By similarity).
-1- SIMILARITY: Belongs to the enclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
B2F95935B2262DE4 CRC64;
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InterPro; IPR000941; Enclase.
Pfam; PF0313; enclase; 1.
Pfam; PF03922; enclase; 1.
PRINTS; PR00148; ENCLASE
ProDom; PD000902; ENCLASE
PROSITE; PS00164; ENCLASE; 1.
PROSITE; PS00164; ENCLASE; 1.
Lyase; Glycolysis; Magnesium; CO ACT SITE 155
MAGMETAL
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ENO OR BL1022.
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Pridmore R.D., Arigoni
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285
312
432 AA;
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10-OCT-2003
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SEQUENCE
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myoglobin gene is transcriptionally active (cardiac and skeletal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Conservative
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01-FEB-1995
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P33363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592
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                                                                                                                                                                                    64 APSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA---- 118
                                                                                                                                                                                                                                                                        119 -RSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGK-----LSFWEAGTTKAGYP-Y 166
                                                                                                                                                                                                                                                                                                                    87 ORALDDLMIELDG------TPNKGKLGANAILGVSLAALYASAESAGLPLY 131
                                                                                        4 YSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSP 63
                                                                                                                                                                                                                              Williams R.S.;
"The winged-helix/forkhead protein myocyte nuclear factor beta (MNF-beta) forms a co-repressor complex with mammalian Sin3B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=P42128-1; Sequence=Displayed;
Name=2; Synonyme=Beta;
Isold=P42128-2; Sequence=VSP 001545, VSP 001546;
-!- TISSUE SPECIFICITY: Expressed in tissues and cells in which the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscles that occur in response to physiological stimuli.
SUBUNIT: Interacts with SIN3B to form a complex which represses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 345:335-343(2000).
-!- FUNCTION: Transcriptional activator that binds to the upstream enhancer region (CCAC box) of myoglobin gene. Has a role in myogenic differentiation and in remodeling processes of adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seldin M.F., Williams R.S.; "Myocyte nuclear factor, a novel winged-helix transcription factor under both developmental and neural regulation in striated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Q., Bassel Duby R., Williams R.S.; "Transient expression of a winged-helix protein, MNF-beta, during
                                                                                                                                                                                                                                                                                                                                                              167 NYNTTASDQLL-----VENAAGHR------VAISTYTTSLGAG 198
                                                                                                                                                                                                                                                                                                                                                                                                           132 RYIGGTNGHILPVPNMNIMNGGAHADFATDIQEYMISPYGFDTYSEALRAG 182
                                                                                                                    |:| ::: | |||:: | || |::|
8 YARQILDSRGNPTVQVVLDTEDGAQGLGL-VPSGASTGEAEA-------
                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
BEDLINE=20088666; PubMed=10620510;
Yang Q., Kong Y., Rothermel B., Garry D.J., Bassel-Duby R.,
Williams R.S.;
7.7%; Score 84; DB 1; Length 432;
19.5%; Pred. No. 7.2;
tive 25; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=94277065; PubMed=8007964;
Bassel-Duby R., Hernandez M.D., Yang Q., Rochelle J.M.,
Seldin M.F., Williams R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PXXI MOUSE STANDARD; PRT; 617 AA. P42128; 035939; 031-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Forkhead box protein K1 (Myocyte nuclear factor) (MNF). Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nyocytes.";
401. Cell. Biol. 14:4596-4605(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401. Cell. Biol. 17:5236-5243(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97415602; PubMed=9271401;
                                                 Conservative
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                         Similarity
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         Local b...
    Query Match
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                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 LTAAEYDQSTYGSSTGPVYVSDSVTLVNVAT-------GAQAVARSLDWTKVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 LDGRPLSTIQQY-SKTFFVLPLRGKLSFWEAGTTKAGYP--YNYNTTASDQLLVENAAGH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1147488; Foxkl.
MGD; MGI:1147488; Foxkl.
GO; GO:0003677; F:DNA binding; IDA.
GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IDA.
InterPro; IPR008984; SMAD_FHA.
InterPro; IPR001766; IF_Fork_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R InterPro; lrkwuller, FRA; 1.

R Pfan; PF00498; FRA; 1.

R Pfan; PF00450; FOXKHEAD.

R PRINTS; PR00053; FOXKHEAD.

DR PRODOM; PR000425; TF FOYK, head; 1.

DR SWART; SW00340; FH; 1.

DR SWART; SW00540; FH; 1.

DR PROSITE; PS00657; FOXK HEAD 1; 1.

DR PROSITE; PS50006; FHA DOWAIN; 1.

DR PROSITE; PS50006; FHA DOWAIN; 1.

DR PROSITE; PS50006; FHA DOWAIN; 1.

RW DNA-binding; Transcription regulation; Activator; Nuclear protein; KW Phosphorylation; Alternative Splicing; Differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 KGIAIPHDIDLGESRVVIQDYDNQHEQDRP-TPSPA-----PSRPFSVLRANDVLWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSPASPTHPG -> SAPASHTSHA (in isoform 2). /FTId=VSP_001545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 83; DB 1; Length 617; 22.4%; Pred. No. 14; Ive 31; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP 001546.
A1083B28C709FC4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 2). /FTId=VSP 001546.
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                                                       SIMILARITY: Contains 1 fork-head domain. SIMILARITY: Contains 1 FHA domain.
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(Rel. 31, Last sequence update)
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-----YTSDYRAAPLPVRAV 606
myocytes, brain, kidney. ...).
PTM: Phosphorylated.
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                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L26507; AAA37529.1; -. EMBL; U95016; AAB69641.1; -. PIR; A56051. A56051. HSSP; Q62245; ZHFH.
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541 TGKPLVLVLMNGRPLALVKEDQQADAI-----LETWFAGTEGGNAIADVLFGDYNPSGK 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 82.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                      FEMS Microbiol. Lett. 72:37-42(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z11535; CAA77633.1; --
PIR; S22134; S22134.
InterPro; IPRO04005; Calici_coat.
Pfam; PF00915; Calici_coat; 1.
Polyprotein; Coat protein.
                                                                                                                                                                                        PRT;
                                                                                                                 652 TVS----DVKLSA 660
                                                                                      192 TTSLGAGPVSISA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11977;
                                                                                                                                                                                                    P274<u>1</u>1;
01-AUG-1992 (
01-AUG-1992 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 APSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VVSANGEPTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQ----DRPTPSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Indels 94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucose.
-1- SUBCELLULAR LOCATION: Periplasmic.
-1- SIMILARITY: Belongs to family 3 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINS-KIZ / MG1653,
STRAINS-KIZ / MG167; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                Periplasmic beta-glucosidase precursor (EC 3.2.1.21) (Gentiobiase)
(Cellobiase) (Beta-D-glucoside glucohydrolase).
BGLX OR B2132.
                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U15049; AAB38487.1; -...
EMBL, U00007; AAA60455.1; ALT_INIT.
EMBL, AE0003022; AAC75193.1; -...
EROGENE; EG12013; bglX.
EcoGene; EG12013; bglX.
InterPro; IPR00172; G1yco_hydro_3C.
InterPro; IPR00175; G1yco_hydro_3N.
Pfam; PF01915; G1yco_hydro_3; 1...
Pfam; PF01915; G1yco_hydro_3; 1...
PROSTIE; PR00173; GLYCOSYL, HYDROL, F3; 1...
Hydrolase; G1ycosidase; Periplasmic; Signal; Complete proteome.
                                                                                                                                                                                                                      STRAIN=K12 / BHB2600;
Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison
                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
Xang M., Luoh S., Goddard A., Reilly D., Henzel W., Bass S.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASMIC BETA-GLUCOSIDASE
BY SIMILARITY.
0E89B0AB42B8F8F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                             Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 T----KVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGT
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   16-OCT-2001 (Rel: 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 83; DB : 19.4%; Pred. No. 18; rative 34; Mismatches
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / BHB2600;
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Best Local Similarity
                                                             Escherichia coli
                                                                                                        NCBI_TaxID=562;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 GAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPY---NYN 169
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                                   ---TKAGYPYN-----YNTTASDOLLVENAA----GHRVAISTY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RPVVSANGEPTV--KLYTSVE-NAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 21, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Non-structural polyprotein [Contains: Coat protein] (Fragment).
Rabbit hemorrhagic disease virus (strain V-351) (RHDV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIINE=22307403; PubMed=1497750;
Milton I.D., Vlasak R., Nowotny N., Rodak L., Carter M.J.;
Milton I.S., terminal sequence comparison of three isolates of rabbit haemorrhagic disease virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ? 234 AA; 23777 MW; B66018654E2EE05A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                              234 AA.
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197 TTLIDLTELIDVRPVGPRPSKSTLVFNLG 225
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